

## SEQUENCE LISTING

IAP5 Rec'd PCT/PTO 10 FEB 2006

&lt;110&gt; TAKARA BIO INC.

&lt;120&gt; Method of decomposing dsRNA and synthesizing RNA

&lt;130&gt; 664674

&lt;150&gt; JP 2003-293553

&lt;151&gt; 2003-08-14

&lt;150&gt; JP 2003-342126

&lt;151&gt; 2003-09-30

&lt;150&gt; JP 2003-409639

&lt;151&gt; 2003-12-08

&lt;150&gt; JP 2004-086129

&lt;151&gt; 2004-03-24

&lt;160&gt; 27

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 1924

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1

Met Lys Ser Pro Ala Leu Gln Pro Leu Ser Met Ala Gly Leu Gln Leu  
 1 5 10 15

Met Thr Pro Ala Ser Ser Pro Met Gly Pro Phe Phe Gly Leu Pro Trp  
 20 25 30

Gln Gln Glu Ala Ile His Asp Asn Ile Tyr Thr Pro Arg Lys Tyr Gln  
 35 40 45

Val Glu Leu Leu Glu Ala Ala Leu Asp His Asn Thr Ile Val Cys Leu  
 50 55 60

Asn Thr Gly Ser Gly Lys Thr Phe Ile Ala Ser Thr Thr Leu Leu Lys  
 65 70 75 80

Ser Cys Leu Tyr Leu Asp Leu Gly Glu Thr Ser Ala Arg Asn Gly Lys

## 664674description (1)Sequence Listing

85

90

95

Arg Thr Val Phe Leu Val Asn Ser Ala Asn Gln Val Ala Gln Gln Val  
 100 105 110

Ser Ala Val Arg Thr His Ser Asp Leu Lys Val Gly Glu Tyr Ser Asn  
 115 120 125

Leu Glu Val Asn Ala Ser Trp Thr Lys Glu Arg Trp Asn Gln Glu Phe  
 130 135 140

Thr Lys His Gln Val Leu Ile Met Thr Cys Tyr Val Ala Leu Asn Val  
 145 150 155 160

Leu Lys Asn Gly Tyr Leu Ser Leu Ser Asp Ile Asn Leu Leu Val Phe  
 165 170 175

Asp Glu Cys His Leu Ala Ile Leu Asp His Pro Tyr Arg Glu Phe Met  
 180 185 190

Lys Leu Cys Glu Ile Cys Pro Ser Cys Pro Arg Ile Leu Gly Leu Thr  
 195 200 205

Ala Ser Ile Leu Asn Gly Lys Trp Asp Pro Glu Asp Leu Glu Glu Lys  
 210 215 220

Phe Gln Lys Leu Glu Lys Ile Leu Lys Ser Asn Ala Glu Thr Ala Thr  
 225 230 235 240

Asp Leu Val Val Leu Asp Arg Tyr Thr Ser Gln Pro Cys Glu Ile Val  
 245 250 255

Val Asp Cys Gly Pro Phe Thr Asp Arg Ser Gly Leu Tyr Glu Arg Leu  
 260 265 270

Leu Met Glu Leu Glu Glu Ala Leu Asn Phe Ile Asn Asp Cys Asn Ile  
 275 280 285

Ser Val His Ser Lys Glu Arg Asp Ser Thr Leu Ile Ser Lys Gln Ile  
 290 295 300

Leu Ser Asp Cys Arg Ala Val Leu Val Val Leu Gly Pro Trp Cys Ala

664674description (1)Sequence Listing  
 305 310 315 320

Asp Lys Val Ala Gly Met Met Val Arg Glu Leu Gln Lys Tyr Ile Lys  
 325 330 335

His Glu Gln Glu Glu Leu His Arg Lys Phe Leu Leu Phe Thr Asp Thr  
 340 345 350

Phe Leu Arg Lys Ile His Ala Leu Cys Glu Glu His Phe Ser Pro Ala  
 355 360 365

Ser Leu Asp Leu Lys Phe Val Thr Pro Lys Val Ile Lys Leu Leu Glu  
 370 375 380

Ile Leu Arg Lys Tyr Lys Pro Tyr Glu Arg His Ser Phe Glu Ser Val  
 385 390 395 400

Glu Trp Tyr Asn Asn Arg Asn Gln Asp Asn Tyr Val Ser Trp Ser Asp  
 405 410 415

Ser Glu Asp Asp Asp Glu Asp Glu Glu Ile Glu Glu Lys Glu Lys Pro  
 420 425 430

Glu Thr Asn Phe Pro Ser Pro Phe Thr Asn Ile Leu Cys Gly Ile Ile  
 435 440 445

Phe Val Glu Arg Arg Tyr Thr Ala Val Val Leu Asn Arg Leu Ile Lys  
 450 455 460

Glu Ala Gly Lys Gln Asp Pro Glu Leu Ala Tyr Ile Ser Ser Asn Phe  
 465 470 475 480

Ile Thr Gly His Gly Ile Gly Lys Asn Gln Pro Arg Asn Asn Thr Met  
 485 490 495

Glu Ala Glu Phe Arg Lys Gln Glu Glu Val Leu Arg Lys Phe Arg Ala  
 500 505 510

His Glu Thr Asn Leu Leu Ile Ala Thr Ser Ile Val Glu Glu Gly Val  
 515 520 525

Asp Ile Pro Lys Cys Asn Leu Val Val Arg Phe Asp Leu Pro Thr Glu

## 664674description (1)Sequence Listing

530

535

540

Tyr Arg Ser Tyr Val Gln Ser Lys Gly Arg Ala Arg Ala Pro Ile Ser  
 545 550 555 560

Asn Tyr Ile Met Leu Ala Asp Thr Asp Lys Ile Lys Ser Phe Glu Glu  
 565 570 575

Asp Leu Lys Thr Tyr Lys Ala Ile Glu Lys Ile Leu Arg Asn Lys Cys  
 580 585 590

Ser Lys Ser Val Asp Thr Gly Glu Thr Asp Ile Asp Pro Val Met Asp  
 595 600 605

Asp Asp His Val Phe Pro Pro Tyr Val Leu Arg Pro Asp Asp Gly Gly  
 610 615 620

Pro Arg Val Thr Ile Asn Thr Ala Ile Gly His Ile Asn Arg Tyr Cys  
 625 630 635 640

Ala Arg Leu Pro Ser Asp Pro Phe Thr His Leu Ala Pro Lys Cys Arg  
 645 650 655

Thr Arg Glu Leu Pro Asp Gly Thr Phe Tyr Ser Thr Leu Tyr Leu Pro  
 660 665 670

Ile Asn Ser Pro Leu Arg Ala Ser Ile Val Gly Pro Pro Met Ser Cys  
 675 680 685

Val Arg Leu Ala Glu Arg Val Val Ala Leu Ile Cys Cys Glu Lys Leu  
 690 695 700

His Lys Ile Gly Glu Leu Asp Asp His Leu Met Pro Val Gly Lys Glu  
 705 710 715 720

Thr Val Lys Tyr Glu Glu Glu Leu Asp Leu His Asp Glu Glu Glu Thr  
 725 730 735

Ser Val Pro Gly Arg Pro Gly Ser Thr Lys Arg Arg Gln Cys Tyr Pro  
 740 745 750

Lys Ala Ile Pro Glu Cys Leu Arg Asp Ser Tyr Pro Arg Pro Asp Gln  
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755

760

765

Pro Cys Tyr Leu Tyr Val Ile Gly Met Val Leu Thr Thr Pro Leu Pro  
 770 775 780

Asp Glu Leu Asn Phe Arg Arg Arg Lys Leu Tyr Pro Pro Glu Asp Thr  
 785 790 795 800

Thr Arg Cys Phe Gly Ile Leu Thr Ala Lys Pro Ile Pro Gln Ile Pro  
 805 810 815

His Phe Pro Val Tyr Thr Arg Ser Gly Glu Val Thr Ile Ser Ile Glu  
 820 825 830

Leu Lys Lys Ser Gly Phe Met Leu Ser Leu Gln Met Leu Glu Leu Ile  
 835 840 845

Thr Arg Leu His Gln Tyr Ile Phe Ser His Ile Leu Arg Leu Glu Lys  
 850 855 860

Pro Ala Leu Glu Phe Lys Pro Thr Asp Ala Asp Ser Ala Tyr Cys Val  
 865 870 875 880

Leu Pro Leu Asn Val Val Asn Asp Ser Ser Thr Leu Asp Ile Asp Phe  
 885 890 895

Lys Phe Met Glu Asp Ile Glu Lys Ser Glu Ala Arg Ile Gly Ile Pro  
 900 905 910

Ser Thr Lys Tyr Thr Lys Glu Thr Pro Phe Val Phe Lys Leu Glu Asp  
 915 920 925

Tyr Gln Asp Ala Val Ile Ile Pro Arg Tyr Arg Asn Phe Asp Gln Pro  
 930 935 940

His Arg Phe Tyr Val Ala Asp Val Tyr Thr Asp Leu Thr Pro Leu Ser  
 945 950 955 960

Lys Phe Pro Ser Pro Glu Tyr Glu Thr Phe Ala Glu Tyr Tyr Lys Thr  
 965 970 975

Lys Tyr Asn Leu Asp Leu Thr Asn Leu Asn Gln Pro Leu Leu Asp Val

664674description (1)Sequence Listing

980

985

990

Asp His Thr Ser Ser Arg Leu Asn Leu Leu Thr Pro Arg His Leu Asn  
995 1000 1005

Gln Lys Gly Lys Ala Leu Pro Leu Ser Ser Ala Glu Lys Arg Lys  
1010 1015 1020

Ala Lys Trp Glu Ser Leu Gln Asn Lys Gln Ile Leu Val Pro Glu  
1025 1030 1035

Leu Cys Ala Ile His Pro Ile Pro Ala Ser Leu Trp Arg Lys Ala  
1040 1045 1050

Val Cys Leu Pro Ser Ile Leu Tyr Arg Leu His Cys Leu Leu Thr  
1055 1060 1065

Ala Glu Glu Leu Arg Ala Gln Thr Ala Ser Asp Ala Gly Val Gly  
1070 1075 1080

Val Arg Ser Leu Pro Ala Asp Phe Arg Tyr Pro Asn Leu Asp Phe  
1085 1090 1095

Gly Trp Lys Lys Ser Ile Asp Ser Lys Ser Phe Ile Ser Ile Ser  
1100 1105 1110

Asn Ser Ser Ser Ala Glu Asn Asp Asn Tyr Cys Lys His Ser Thr  
1115 1120 1125

Ile Val Pro Glu Asn Ala Ala His Gln Gly Ala Asn Arg Thr Ser  
1130 1135 1140

Ser Leu Glu Asn His Asp Gln Met Ser Val Asn Cys Arg Thr Leu  
1145 1150 1155

Leu Ser Glu Ser Pro Gly Lys Leu His Val Glu Val Ser Ala Asp  
1160 1165 1170

Leu Thr Ala Ile Asn Gly Leu Ser Tyr Asn Gln Asn Leu Ala Asn  
1175 1180 1185

Gly Ser Tyr Asp Leu Ala Asn Arg Asp Phe Cys Gln Gly Asn Gln

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1190		1195		1200
Leu Asn Tyr Tyr Lys Gln Glu Ile Pro Val Gln Pro Thr Thr Ser	1205	1210	1215	
Tyr Ser Ile Gln Asn Leu Tyr Ser Tyr Glu Asn Gln Pro Gln Pro	1220	1225	1230	
Ser Asp Glu Cys Thr Leu Leu Ser Asn Lys Tyr Leu Asp Gly Asn	1235	1240	1245	
Ala Asn Lys Ser Thr Ser Asp Gly Ser Pro Val Met Ala Val Met	1250	1255	1260	
Pro Gly Thr Thr Asp Thr Ile Gln Val Leu Lys Gly Arg Met Asp	1265	1270	1275	
Ser Glu Gln Ser Pro Ser Ile Gly Tyr Ser Ser Arg Thr Leu Gly	1280	1285	1290	
Pro Asn Pro Gly Leu Ile Leu Gln Ala Leu Thr Leu Ser Asn Ala	1295	1300	1305	
Ser Asp Gly Phe Asn Leu Glu Arg Leu Glu Met Leu Gly Asp Ser	1310	1315	1320	
Phe Leu Lys His Ala Ile Thr Thr Tyr Leu Phe Cys Thr Tyr Pro	1325	1330	1335	
Asp Ala His Glu Gly Arg Leu Ser Tyr Met Arg Ser Lys Lys Val	1340	1345	1350	
Ser Asn Cys Asn Leu Tyr Arg Leu Gly Lys Lys Lys Gly Leu Pro	1355	1360	1365	
Ser Arg Met Val Val Ser Ile Phe Asp Pro Pro Val Asn Trp Leu	1370	1375	1380	
Pro Pro Gly Tyr Val Val Asn Gln Asp Lys Ser Asn Thr Asp Lys	1385	1390	1395	
Trp Glu Lys Asp Glu Met Thr Lys Asp Cys Met Leu Ala Asn Gly				

## 1410

Lys	Leu	Asp	Glu	Asp	Tyr	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Ser
1415						1420				1425			
Leu	Met	Trp	Arg	Ala	Pro	Lys	Glu	Glu	Ala	Asp	Tyr	Glu	Asp
1430						1435					1440		Asp
Phe	Leu	Glu	Tyr	Asp	Gln	Glu	His	Ile	Arg	Phe	Ile	Asp	Asn
1445						1450					1455		Met
Leu	Met	Gly	Ser	Gly	Ala	Phe	Val	Lys	Lys	Ile	Ser	Leu	Ser
1460						1465					1470		Pro
Phe	Ser	Thr	Thr	Asp	Ser	Ala	Tyr	Glu	Trp	Lys	Met	Pro	Lys
1475						1480					1485		Lys
Ser	Ser	Leu	Gly	Ser	Met	Pro	Phe	Ser	Ser	Asp	Phe	Glu	Asp
1490						1495					1500		Phe
Asp	Tyr	Ser	Ser	Trp	Asp	Ala	Met	Cys	Tyr	Leu	Asp	Pro	Ser
1505						1510					1515		Lys
Ala	Val	Glu	Glu	Asp	Asp	Phe	Val	Val	Gly	Phe	Trp	Asn	Pro
1520						1525					1530		Ser
Glu	Glu	Asn	Cys	Gly	Val	Asp	Thr	Gly	Lys	Gln	Ser	Ile	Ser
1535						1540					1545		Tyr
Asp	Leu	His	Thr	Glu	Gln	Cys	Ile	Ala	Asp	Lys	Ser	Ile	Ala
1550						1555					1560		Asp
Cys	Val	Glu	Ala	Leu	Leu	Gly	Cys	Tyr	Leu	Thr	Ser	Cys	Gly
1565						1570					1575		Glu
Arg	Ala	Ala	Gln	Leu	Phe	Leu	Cys	Ser	Leu	Gly	Leu	Lys	Val
1580						1585					1590		Leu
Pro	Val	Ile	Lys	Arg	Thr	Asp	Arg	Glu	Lys	Ala	Leu	Cys	Pro
1595						1600					1605		Thr



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Arg	Glu	Asn	Phe	Asn	Ser	Gln	Gln	Lys	Asn	Leu	Ser	Val	Ser	Cys
1610						1615					1620			
Ala	Ala	Ala	Ser	Val	Ala	Ser	Ser	Arg	Ser	Ser	Val	Leu	Lys	Asp
1625						1630					1635			
Ser	Glu	Tyr	Gly	Cys	Leu	Lys	Ile	Pro	Pro	Arg	Cys	Met	Phe	Asp
1640						1645					1650			
His	Pro	Asp	Ala	Asp	Lys	Thr	Leu	Asn	His	Leu	Ile	Ser	Gly	Phe
1655						1660					1665			
Glu	Asn	Phe	Glu	Lys	Lys	Ile	Asn	Tyr	Arg	Phe	Lys	Asn	Lys	Ala
1670						1675					1680			
Tyr	Leu	Leu	Gln	Ala	Phe	Thr	His	Ala	Ser	Tyr	His	Tyr	Asn	Thr
1685						1690					1695			
Ile	Thr	Asp	Cys	Tyr	Gln	Arg	Leu	Glu	Phe	Leu	Gly	Asp	Ala	Ile
1700						1705					1710			
Leu	Asp	Tyr	Leu	Ile	Thr	Lys	His	Leu	Tyr	Glu	Asp	Pro	Arg	Gln
1715						1720					1725			
His	Ser	Pro	Gly	Val	Leu	Thr	Asp	Leu	Arg	Ser	Ala	Leu	Val	Asn
1730						1735					1740			
Asn	Thr	Ile	Phe	Ala	Ser	Leu	Ala	Val	Lys	Tyr	Asp	Tyr	His	Lys
1745						1750					1755			
Tyr	Phe	Lys	Ala	Val	Ser	Pro	Glu	Leu	Phe	His	Val	Ile	Asp	Asp
1760						1765					1770			
Phe	Val	Gln	Phe	Gln	Leu	Glu	Lys	Asn	Glu	Met	Gln	Gly	Met	Asp
1775						1780					1785			
Ser	Glu	Leu	Arg	Arg	Ser	Glu	Glu	Asp	Glu	Glu	Lys	Glu	Glu	Asp
1790						1795					1800			
Ile	Glu	Val	Pro	Lys	Ala	Met	Gly	Asp	Ile	Phe	Glu	Ser	Leu	Ala
1805						1810					1815			

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Gly Ala Ile Tyr Met Asp Ser Gly Met Ser Leu Glu Thr Val Trp  
1820 1825 1830

Gln Val Tyr Tyr Pro Met Met Arg Pro Leu Ile Glu Lys Phe Ser  
1835 1840 1845

Ala Asn Val Pro Arg Ser Pro Val Arg Glu Leu Leu Glu Met Glu  
1850 1855 1860

Pro Glu Thr Ala Lys Phe Ser Pro Ala Glu Arg Thr Tyr Asp Gly  
1865 1870 1875

Lys Val Arg Val Thr Val Glu Val Val Gly Lys Gly Lys Phe Lys  
1880 1885 1890

Gly Val Gly Arg Ser Tyr Arg Ile Ala Lys Ser Ala Ala Ala Arg  
1895 1900 1905

Arg Ala Leu Arg Ser Leu Lys Ala Asn Gln Pro Gln Val Pro Asn  
1910 1915 1920

Ser

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<211> 5772  
<212> DNA  
<213> Homo sapiens

<400> 2  
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tcctcaccaa tgggtccttt ctttggactg ccatggcaac aagaagcaat tcataataac 120  
atttatacgc caagaaaata tcaggttgaa ctgcttgaag cagctctgga tcataataac 180  
atcgtctgtt taaacactgg ctgagggaag acatttattg ctagtactac tctactaaag 240  
agctgtctct atctagatct aggggagact tcagctagaa atggaaaaag gacgggtgtt 300  
ttggtcaact ctgcaaacca ggttgcotcaa caagtgtcag ctgtcagaac tcattcagat 360  
ctcaagggtg gggaatactc aaacctagaa gtaaattgat cttggacaaa agagagatgg 420  
aaccaagagt ttactaagca ccaggttctc attatgactt gctatgtcgc cttgaatgtt 480  
ttgaaaaatg gttacttata actgtcagac attaaccttt tgggtgttga tgagtgtcat 540

664674description (1)Sequence Listing

cttgcaatcc tagaccaccc ctatcgagaa tttatgaagc tctgtgaaat ttgtccatca	600
tgtcctcgca ttttgggact aactgcttcc attttaaagtg ggaaatggga tocagaggat	660
ttggaagaaa agtttcagaa actagagaaa attottaaga gtaatgctga aactgcaact	720
gacctggttg tottagacag gtatacttct cagccatgtg agattgtggt ggattgtgga	780
ccattttactg acagaagtgg gctttatgaa agactgctga tggaattaga agaagcactt	840
aattttatca atgattgtaa tatactgtga cattcaaaag aaagagattc tactttaatt	900
tcgaaacaga tactatcaga ctgtcgtgcc gtattggtag ttctgggacc ctggtgtgca	960
gataaagtag ctggaatgat ggtaagagaa ctacagaaat acatcaaaca tgagcaagag	1020
gagctgcaca ggaaattttt attgtttaca gacactttcc taaggaaaat acatgcacta	1080
tgtgaagagc acttctcacc tgcctcactt gacctgaaat ttgtaactcc taaagtaatc	1140
aaactgctcg aaatcttacg caaatataaa ccatatgagc gacacagttt tgaaagcgtt	1200
gagtgttata ataatagaaa tcaggataat tatgtgtcat ggagtgattc tgaggatgat	1260
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agattgataa aggaagctgg caaacaagat ccagagctgg cttatatcag tagcaatttc	1440
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gotagattac caagtgatcc gtttactcat ctagctccta aatgcagaac ccgagagttg	1980
cctgatggta catttttatt aactctttat ctgccaatta actcacctct tcgagcctcc	2040
attgttggtc caccaatgag ctgtgtacga ttggctgaaa gagttgtcgc tctcatttgc	2100
tgtgagaaac tgcacaaaat tggcgaactg gatgaccatt tgatgccagt tgggaaagag	2160
actgttaaat atgaagagga gcttgatttg catgatgaag aagagaccag tgttccagga	2220

## 664674description (1)Sequence Listing

agaccagggtt ccaogaaacg aaggcagtg	tacccaaaag caattccaga gtgtttgagg	2280
gatagttatc ccagacctga tcagccctgt	tacctgtatg tgataggaat ggttttaact	2340
acacctttac ctgatgaact caactttaga	aggcggaagc tctatcctcc tgaagatacc	2400
acaagatgct ttggaatact gacggccaaa	cccatacctc agattccaca ctttcctgtg	2460
tacacacgct ctggagaggt taccatatcc	attgagtiga agaagtctgg tttcatgttg	2520
tctctacaaa tgcttgagtt gattacaaga	cttcaccagt atatattctc acatattctt	2580
cggcttgaaa aacctgcact agaatttaaa	cctacagacg ctgattcagc atactgtgtt	2640
ctacctctta atgttggttaa tgactccagc	actttggata ttgactttaa attcatggaa	2700
gatattgaga agtctgaagc tcgcataggc	attcccagta caaagtatac aaaagaaaca	2760
ccctttgttt ttaaattaga agattaccaa	gatgccgtta tcattccaag atatcgcaat	2820
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aaatttcctt cccctgagta tgaaactttt	gcagaatatt ataaaacaaa gtacaacctt	2940
gacctaacca atctcaacca gccactgctg	gatgtggacc acacatcttc aagacttaat	3000
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gccgtaatgc ctggtacgac agacactatt	caagtgtca agggcaggat ggattctgag	3840
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## 664674description (1)Sequence Listing

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cggccactaa tagaaaagtt ttctgcaaat gtaccccggt cccctgtgog agaattgctt	5580

664674description (1)Sequence Listing

gaaatggaac cagaaactgc caaatttagc cggctgaga gaacttacga cggaaggtc	5640
agagtcactg tggaagtagt aggaaagggg aaatttaaag gtgttggtcg aagttacagg	5700
attgccaaat ctgcagcagc aagaagagcc ctccgaagcc tcaaagctaa tcaacctcag	5760
gttcccaata gc	5772

<210> 3  
 <211> 1962  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> A gene encoding human dicer mutant

<400> 3	
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ggatttaacc tggagcggct tgaaatgctt ggcgactcct ttttaaagca tgccatcacc	180
acatatctat tttgcactta ccctgatgcg catgagggcc gcctttcata tatgagaagc	240
aaaaaggtca gcaactgtaa tctgtatcgc cttggaaaaa agaagggact acccagccgc	300
atggtggtgt caatatttga tccccctgtg aattggcttc ctcttggtta ttagtaaat	360
caagacaaaa gcaacacaga taaatgggaa aaagatgaaa tgacaaaaga ctgcatgctg	420
gcgaatggca aactggatga ggattacgag gaggaggatg aggaggagga gagcctgatg	480
tggagggctc cgaaggaaga ggctgactat gaagatgatt tcctggagta tgatcaggaa	540
catatcagat ttatagataa tatgttaatg gggtcaggag cttttgtaaa gaaaatctct	600
ctttctcctt tttcaaccac tgattctgca tatgaatgga aaatgcccac aaaatcctcc	660
ttaggtagta tgccattttc atcagatttt gaggattttg actacagctc ttgggatgca	720
atgtgctatc tggatcctag caaagctgtt gaagaagatg actttgttgt ggggttctgg	780
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cacactgagc agtgtattgc tgacaaaagc atagcggact gtgtggaagc cctgctgggc	900
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aatttcaaca gccacaaaa gaacctttca gtgagctgtg ctgctgcttc tgtggccagt	1080
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# 664674description (1)Sequence Listing

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atgtttgata atccagatgc agataaaaca ctgaatcacc ttatatcggg gtttgaaaat 1200
tttgaaaaga aaatcaacta cagattcaag aataaggctt accttctcca ggcttttaca 1260
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ccggctgaga gaacttacga cgggaaggtc agagtcactg tggaagtagt aggaaagggg 1860
aaatttaaag gtgttggtcg aagttacagg attgccaaat ctgcagcagc aagaagagcc 1920
ctccgaagcc tcaaagctaa tcaacctcag gttccaata gc 1962

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<210> 4

<211> 654

<212> PRT

<213> Artificial sequence

<220>

<223> An amino acid sequence of human dicer mutant.

<400> 4

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Gln Val Leu Lys Gly Arg Met Asp Ser Glu Gln Ser Pro Ser Ile Gly
1          5          10          15

```

```

Tyr Ser Ser Arg Thr Leu Gly Pro Asn Pro Gly Leu Ile Leu Gln Ala
20          25          30

```

```

Leu Thr Leu Ser Asn Ala Ser Asp Gly Phe Asn Leu Glu Arg Leu Glu
35          40          45

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Met Leu Gly Asp Ser Phe Leu Lys His Ala Ile Thr Thr Tyr Leu Phe
50          55          60

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664674description (1)Sequence Listing

Cys Thr Tyr Pro Asp Ala His Glu Gly Arg Leu Ser Tyr Met Arg Ser  
65 70 75 80

Lys Lys Val Ser Asn Cys Asn Leu Tyr Arg Leu Gly Lys Lys Lys Gly  
85 90 95

Leu Pro Ser Arg Met Val Val Ser Ile Phe Asp Pro Pro Val Asn Trp  
100 105 110

Leu Pro Pro Gly Tyr Val Val Asn Gln Asp Lys Ser Asn Thr Asp Lys  
115 120 125

Trp Glu Lys Asp Glu Met Thr Lys Asp Cys Met Leu Ala Asn Gly Lys  
130 135 140

Leu Asp Glu Asp Tyr Glu Glu Glu Asp Glu Glu Glu Glu Ser Leu Met  
145 150 155 160

Trp Arg Ala Pro Lys Glu Glu Ala Asp Tyr Glu Asp Asp Phe Leu Glu  
165 170 175

Tyr Asp Gln Glu His Ile Arg Phe Ile Asp Asn Met Leu Met Gly Ser  
180 185 190

Gly Ala Phe Val Lys Lys Ile Ser Leu Ser Pro Phe Ser Thr Thr Asp  
195 200 205

Ser Ala Tyr Glu Trp Lys Met Pro Lys Lys Ser Ser Leu Gly Ser Met  
210 215 220

Pro Phe Ser Ser Asp Phe Glu Asp Phe Asp Tyr Ser Ser Trp Asp Ala  
225 230 235 240

Met Cys Tyr Leu Asp Pro Ser Lys Ala Val Glu Glu Asp Asp Phe Val  
245 250 255

Val Gly Phe Trp Asn Pro Ser Glu Glu Asn Cys Gly Val Asp Thr Gly  
260 265 270

Lys Gln Ser Ile Ser Tyr Asp Leu His Thr Glu Gln Cys Ile Ala Asp  
275 280 285



664674description (1)Sequence Listing  
 Lys Ser Ile Ala Asp Cys Val Glu Ala Leu Leu Gly Cys Tyr Leu Thr  
 290 295 300

Ser Cys Gly Glu Arg Ala Ala Gln Leu Phe Leu Cys Ser Leu Gly Leu  
 305 310 315 320

Lys Val Leu Pro Val Ile Lys Arg Thr Asp Arg Glu Lys Ala Leu Cys  
 325 330 335

Pro Thr Arg Glu Asn Phe Asn Ser Gln Gln Lys Asn Leu Ser Val Ser  
 340 345 350

Cys Ala Ala Ala Ser Val Ala Ser Ser Arg Ser Ser Val Leu Lys Asp  
 355 360 365

Ser Glu Tyr Gly Cys Leu Lys Ile Pro Pro Arg Cys Met Phe Asp His  
 370 375 380

Pro Asp Ala Asp Lys Thr Leu Asn His Leu Ile Ser Gly Phe Glu Asn  
 385 390 395 400

Phe Glu Lys Lys Ile Asn Tyr Arg Phe Lys Asn Lys Ala Tyr Leu Leu  
 405 410 415

Gln Ala Phe Thr His Ala Ser Tyr His Tyr Asn Thr Ile Thr Asp Cys  
 420 425 430

Tyr Gln Arg Leu Glu Phe Leu Gly Asp Ala Ile Leu Asp Tyr Leu Ile  
 435 440 445

Thr Lys His Leu Tyr Glu Asp Pro Arg Gln His Ser Pro Gly Val Leu  
 450 455 460

Thr Asp Leu Arg Ser Ala Leu Val Asn Asn Thr Ile Phe Ala Ser Leu  
 465 470 475 480

Ala Val Lys Tyr Asp Tyr His Lys Tyr Phe Lys Ala Val Ser Pro Glu  
 485 490 495

Leu Phe His Val Ile Asp Asp Phe Val Gln Phe Gln Leu Glu Lys Asn  
 500 505 510

664674description (1)Sequence Listing

Glu Met Gln Gly Met Asp Ser Glu Leu Arg Arg Ser Glu Glu Asp Glu  
515 520 525

Glu Lys Glu Glu Asp Ile Glu Val Pro Lys Ala Met Gly Asp Ile Phe  
530 535 540

Glu Ser Leu Ala Gly Ala Ile Tyr Met Asp Ser Gly Met Ser Leu Glu  
545 550 555 560

Thr Val Trp Gln Val Tyr Tyr Pro Met Met Arg Pro Leu Ile Glu Lys  
565 570 575

Phe Ser Ala Asn Val Pro Arg Ser Pro Val Arg Glu Leu Leu Glu Met  
580 585 590

Glu Pro Glu Thr Ala Lys Phe Ser Pro Ala Glu Arg Thr Tyr Asp Gly  
595 600 605

Lys Val Arg Val Thr Val Glu Val Val Gly Lys Gly Lys Phe Lys Gly  
610 615 620

Val Gly Arg Ser Tyr Arg Ile Ala Lys Ser Ala Ala Ala Arg Arg Ala  
625 630 635 640

Leu Arg Ser Leu Lys Ala Asn Gln Pro Gln Val Pro Asn Ser  
645 650

<210> 5

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic primer 1 to amplify a gene encoding human dicer

<400> 5

tcgagctcgg tacccaagt gctcaagggc aggatg

36

<210> 6

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic primer 2 to amplify a gene encoding human dicer

# 664674description (1)Sequence Listing

<400> 6  
tatctagaaa gcttttagct attggaacc tgaggt 36

<210> 7  
<211> 42  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic primer 3 to amplify a gene encoding red-shifted green fluorescence protein

<400> 7  
gggtaatacg actcactata gggagaatgg ctagcaaagg ag 42

<210> 8  
<211> 42  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic primer 4 to amplify a gene encoding red-shifted green fluorescence protein

<400> 8  
gggtaatacg actcactata gggagatcag ttgtacagtt ca 42

<210> 9  
<211> 66  
<212> PRT  
<213> Thermotoga maritima

<400> 9

Met Arg Gly Lys Val Lys Trp Phe Asp Ser Lys Lys Gly Tyr Gly Phe  
1 5 10 15

Ile Thr Lys Asp Glu Gly Gly Asp Val Phe Val His Trp Ser Ala Ile  
20 25 30

Glu Met Glu Gly Phe Lys Thr Leu Lys Glu Gly Gln Val Val Glu Phe  
35 40 45

Glu Ile Gln Glu Gly Lys Lys Gly Pro Gln Ala Ala His Val Lys Val  
50 55 60

Val Glu  
65

# 664674description (1)Sequence Listing

<210> 10  
 <211> 198  
 <212> DNA  
 <213> Thermotoga maritima

<400> 10  
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 gaaggaggag acgtgttcgt aacttggtca gccatcgaaa tggaagggtt caaaactctg 120  
 aaggaaggcc aggtogtoga gttcgagatt caggaaggca agaaagggtcc acaggcagcg 180  
 cacgtgaaag tagttgag 198

<210> 11  
 <211> 720  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> A gene encoding red-shifted green fluorescence protein.

<400> 11  
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 ggtgatgtta acggccacaa gttctctgtc agtggagagg gtgaaggatga tgcaacatac 120  
 ggaaaactta ccctgaagtt catctgcact actggcaaac tgctgtttcc atggccaaca 180  
 ctagtcaacta ctotgtgcta tgggtgttcaa tgcttttcaa gatacccgga tcatatgaaa 240  
 cggcatgact ttttcaagag tgccatgccc gaaggttatg tacaggaaag gaccatcttc 300  
 ttcaaagatg acggcaacta caagacacgt gctgaagtca agtttgaagg tgataccott 360  
 gttaatagaa tcgagttaaa aggtattgac ttcaaggaag atggaaacat totgggacac 420  
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 ggaatcaaag tgaacttcaa gaccgcccac aacattgaag atggaagcgt tcaactagca 540  
 gaccattatc aacaaaatac tccaattggc gatggccctg tccttttacc agacaacat 600  
 tacctgtcca cacaatctgc cttttcgaaa gatcccaacg aaaagagaga ccacatggtc 660  
 ottottgagt ttgtaacagc tgctgggatt acacatggca tggatgaact gtacaactga 720

<210> 12  
 <211> 675  
 <212> PRT  
 <213> Artificial sequence

<220>

664674description (1)Sequence Listing

<223> An amino acid sequence of human dicer mutant

<400> 12

Met Asn His Lys Val His His His His His His Ile Glu Gly Arg Asn  
1 5 10 15

Ser Ser Ser Val Pro Gln Val Leu Lys Gly Arg Met Asp Ser Glu Gln  
20 25 30

Ser Pro Ser Ile Gly Tyr Ser Ser Arg Thr Leu Gly Pro Asn Pro Gly  
35 40 45

Leu Ile Leu Gln Ala Leu Thr Leu Ser Asn Ala Ser Asp Gly Phe Asn  
50 55 60

Leu Glu Arg Leu Glu Met Leu Gly Asp Ser Phe Leu Lys His Ala Ile  
65 70 75 80

Thr Thr Tyr Leu Phe Cys Thr Tyr Pro Asp Ala His Glu Gly Arg Leu  
85 90 95

Ser Tyr Met Arg Ser Lys Lys Val Ser Asn Cys Asn Leu Tyr Arg Leu  
100 105 110

Gly Lys Lys Lys Gly Leu Pro Ser Arg Met Val Val Ser Ile Phe Asp  
115 120 125

Pro Pro Val Asn Trp Leu Pro Pro Gly Tyr Val Val Asn Gln Asp Lys  
130 135 140

Ser Asn Thr Asp Lys Trp Glu Lys Asp Glu Met Thr Lys Asp Cys Met  
145 150 155 160

Leu Ala Asn Gly Lys Leu Asp Glu Asp Tyr Glu Glu Glu Asp Glu Glu  
165 170 175

Glu Glu Ser Leu Met Trp Arg Ala Pro Lys Glu Glu Ala Asp Tyr Glu  
180 185 190

Asp Asp Phe Leu Glu Tyr Asp Gln Glu His Ile Arg Phe Ile Asp Asn  
195 200 205

664674description (1)Sequence Listing

Met Leu Met Gly Ser Gly Ala Phe Val Lys Lys Ile Ser Leu Ser Pro  
210 215 220

Phe Ser Thr Thr Asp Ser Ala Tyr Glu Trp Lys Met Pro Lys Lys Ser  
225 230 235 240

Ser Leu Gly Ser Met Pro Phe Ser Ser Asp Phe Glu Asp Phe Asp Tyr  
245 250 255

Ser Ser Trp Asp Ala Met Cys Tyr Leu Asp Pro Ser Lys Ala Val Glu  
260 265 270

Glu Asp Asp Phe Val Val Gly Phe Trp Asn Pro Ser Glu Glu Asn Cys  
275 280 285

Gly Val Asp Thr Gly Lys Gln Ser Ile Ser Tyr Asp Leu His Thr Glu  
290 295 300

Gln Cys Ile Ala Asp Lys Ser Ile Ala Asp Cys Val Glu Ala Leu Leu  
305 310 315 320

Gly Cys Tyr Leu Thr Ser Cys Gly Glu Arg Ala Ala Gln Leu Phe Leu  
325 330 335

Cys Ser Leu Gly Leu Lys Val Leu Pro Val Ile Lys Arg Thr Asp Arg  
340 345 350

Glu Lys Ala Leu Cys Pro Thr Arg Glu Asn Phe Asn Ser Gln Gln Lys  
355 360 365

Asn Leu Ser Val Ser Cys Ala Ala Ala Ser Val Ala Ser Ser Arg Ser  
370 375 380

Ser Val Leu Lys Asp Ser Glu Tyr Gly Cys Leu Lys Ile Pro Pro Arg  
385 390 395 400

Cys Met Phe Asp His Pro Asp Ala Asp Lys Thr Leu Asn His Leu Ile  
405 410 415

Ser Gly Phe Glu Asn Phe Glu Lys Lys Ile Asn Tyr Arg Phe Lys Asn  
420 425 430

664674description (1)Sequence Listing

Lys Ala Tyr Leu Leu Gln Ala Phe Thr His Ala Ser Tyr His Tyr Asn  
           435                          440                          445  
  
 Thr Ile Thr Asp Cys Tyr Gln Arg Leu Glu Phe Leu Gly Asp Ala Ile  
           450                          455                          460  
  
 Leu Asp Tyr Leu Ile Thr Lys His Leu Tyr Glu Asp Pro Arg Gln His  
           465                          470                          475                          480  
  
 Ser Pro Gly Val Leu Thr Asp Leu Arg Ser Ala Leu Val Asn Asn Thr  
                           485                          490                          495  
  
 Ile Phe Ala Ser Leu Ala Val Lys Tyr Asp Tyr His Lys Tyr Phe Lys  
                           500                          505                          510  
  
 Ala Val Ser Pro Glu Leu Phe His Val Ile Asp Asp Phe Val Gln Phe  
           515                          520                          525  
  
 Gln Leu Glu Lys Asn Glu Met Gln Gly Met Asp Ser Glu Leu Arg Arg  
           530                          535                          540  
  
 Ser Glu Glu Asp Glu Glu Lys Glu Glu Asp Ile Glu Val Pro Lys Ala  
           545                          550                          555                          560  
  
 Met Gly Asp Ile Phe Glu Ser Leu Ala Gly Ala Ile Tyr Met Asp Ser  
                           565                          570                          575  
  
 Gly Met Ser Leu Glu Thr Val Trp Gln Val Tyr Tyr Pro Met Met Arg  
                           580                          585                          590  
  
 Pro Leu Ile Glu Lys Phe Ser Ala Asn Val Pro Arg Ser Pro Val Arg  
           595                          600                          605  
  
 Glu Leu Leu Glu Met Glu Pro Glu Thr Ala Lys Phe Ser Pro Ala Glu  
           610                          615                          620  
  
 Arg Thr Tyr Asp Gly Lys Val Arg Val Thr Val Glu Val Val Gly Lys  
           625                          630                          635                          640  
  
 Gly Lys Phe Lys Gly Val Gly Arg Ser Tyr Arg Ile Ala Lys Ser Ala  
           645                          650                          655

664674description (1)Sequence Listing

Ala Ala Arg Arg Ala Leu Arg Ser Leu Lys Ala Asn Gln Pro Gln Val  
660 665 670

Pro Asn Ser  
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<210> 13  
<211> 2025  
<212> DNA  
<213> Artificial sequence

<220>  
<223> A gene encoding human dicer mutant

<400> 13  
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ctgaaggtgc tcccggtaat taaaaggact gatcgggaaa aggccctgtg ccctactcgg 1080  
gagaatttca acagccaaca aaagaacctt tcagttagct gtgctgctgc ttctgtggcc 1140



## 664674description (1)Sequence Listing

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agttcacgct cttctgtatt gaaagactcg gaatatgggt gtttgaagat tccaccaaga 1200
tgtatgtttg atcatccaga tgcagataaa aactgaatc accttatatc ggggtttgaa 1260
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gagcttagga gatctgagga ggatgaagag aaagaagagg atattgaagt tccaaaggcc 1680
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agcccggctg agagaactta cgacgggaag gtcagagtca ctgtggaagt agtaggaaag 1920
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gccctccgaa gcctcaaagc taatcaacct caggttccca atagc 2025

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<210> 14  
 <211> 36  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Synthetic primer 5 to amplify a gene encoding human dicer mutant

<400> 14  
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<210> 15  
 <211> 36  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Synthetic primer 6 to amplify a gene encoding human dicer mutant

<400> 15  
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<210> 16  
 <211> 3741

## 664674description (1)Sequence Listing

<212> DNA  
 <213> Artificial

<220>  
 <223> A gene encoding human dicer mutant

<400> 16  
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 aaagagactg ttaaataatga agaggagcctt gatttgcattg atgaagaaga gaccagtgtt 180  
 ccaggaagac caggttccac gaaacgaagg cagtgtctacc caaaagcaat tccagagtgt 240  
 ttgagggata gttatcccag acctgatcag ccctgttacc tgtatgtgat aggaatgggt 300  
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 gaaaatgata attactgtaa gcacagcaca attgtccctg aaaatgctgc acatcaaggt 1380  
 gctaatagaa cctcctctct agaaaatcat gaccaaagt ctgtgaactg cagaacgttg 1440  
 ctcagcgagt cccctggtaa gctccacgtt gaagtttcag cagatcttac agcaattaat 1500

## 664674description (1)Sequence Listing

ggtcttttctt acaatcaaaa tctcgccaat ggcagttatg atttagctaa cagagacttt	1560
tgccaaggaa atcagctaaa ttactacaag caggaaatac ccgtgcaacc aactacctca	1620
tattccattc agaatttata cagttacgag aaccagcccc agcccagcga tgaatgtact	1680
ctcctgagta ataaatacct tgatggaaat gctaacaaat ctacctcaga tggaagtcct	1740
gtgatggcog taatgcctgg tacgacagac actattcaag tgctcaaggg caggatggat	1800
tctgagcaga gcccttttat tgggtactcc tcaaggactc ttggcccaa toctggactt	1860
attcttcagg ctttgactct gtcaaacgct agtgatggat ttaacctgga ggggcttgaa	1920
atgcttggcg actccttttt aaagcatgcc atcaccacat atctattttg cacttaccct	1980
gatgcgcattg agggccgcct ttcatatatg agaagcaaaa aggtcagcaa ctgtaatctg	2040
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cctgtgaatt ggcttctcc tggttatgta gtaaatacag acaaaagcaa cacagataaa	2160
tgggaaaaag atgaaatgac aaaagactgc atgctggcga atggcaaact ggatgaggat	2220
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gactatgaag atgatttcct ggagtatgat caggaacata tcagatttat agataatatg	2340
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tctgcatatg aatggaaaat gcccaaaaaa tctccttag gtagtatgcc attttcatca	2460
gattttgagg attttgacta cagctcttgg gatgcaatgt gctatctgga tcctagcaaa	2520
gctgttgaag aagatgactt tgttggtgggg ttctggaatc catcagaaga aaactgtggt	2580
gttgacacgg gaaagcagtc catttcttac gacttgaca ctgagcagtg tattgctgac	2640
aaaagcatag cggactgtgt ggaagccctg ctgggctgct atttaaccag ctgtggggag	2700
agggtgctc agcttttctt ctgttcactg gggctgaagg tgctcccgtt aattaaaagg	2760
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accaagcacc tttatgaaga cccgcggcag cactccccgg gggctcctgac agacctgcgg	3180

# 664674description (1)Sequence Listing

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aaggtcagag tcaactgtga agtagtagga aaggggaaat ttaaagggtg tggtcgaagt 3660
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cctcaggttc ccaatagcta a 3741
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<210> 17  
 <211> 1246  
 <212> PRT  
 <213> Artificial

<220>  
 <223> An amino acid sequence of human dicer mutant

<400> 17

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Ala Ser Ile Val Gly Pro Pro Met Ser Cys Val Arg Leu Ala Glu Arg
1 5 10 15
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```
Val Val Ala Leu Ile Cys Cys Glu Lys Leu His Lys Ile Gly Glu Leu
20 25 30
```

```
Asp Asp His Leu Met Pro Val Gly Lys Glu Thr Val Lys Tyr Glu Glu
35 40 45
```

```
Glu Leu Asp Leu His Asp Glu Glu Glu Thr Ser Val Pro Gly Arg Pro
50 55 60
```

```
Gly Ser Thr Lys Arg Arg Gln Cys Tyr Pro Lys Ala Ile Pro Glu Cys
65 70 75 80
```

```
Leu Arg Asp Ser Tyr Pro Arg Pro Asp Gln Pro Cys Tyr Leu Tyr Val
85 90 95
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664674description (1)Sequence Listing

Ile Gly Met Val Leu Thr Thr Pro Leu Pro Asp Glu Leu Asn Phe Arg  
100 105 110

Arg Arg Lys Leu Tyr Pro Pro Glu Asp Thr Thr Arg Cys Phe Gly Ile  
115 120 125

Leu Thr Ala Lys Pro Ile Pro Gln Ile Pro His Phe Pro Val Tyr Thr  
130 135 140

Arg Ser Gly Glu Val Thr Ile Ser Ile Glu Leu Lys Lys Ser Gly Phe  
145 150 155 160

Met Leu Ser Leu Gln Met Leu Glu Leu Ile Thr Arg Leu His Gln Tyr  
165 170 175

Ile Phe Ser His Ile Leu Arg Leu Glu Lys Pro Ala Leu Glu Phe Lys  
180 185 190

Pro Thr Asp Ala Asp Ser Ala Tyr Cys Val Leu Pro Leu Asn Val Val  
195 200 205

Asn Asp Ser Ser Thr Leu Asp Ile Asp Phe Lys Phe Met Glu Asp Ile  
210 215 220

Glu Lys Ser Glu Ala Arg Ile Gly Ile Pro Ser Thr Lys Tyr Thr Lys  
225 230 235 240

Glu Thr Pro Phe Val Phe Lys Leu Glu Asp Tyr Gln Asp Ala Val Ile  
245 250 255

Ile Pro Arg Tyr Arg Asn Phe Asp Gln Pro His Arg Phe Tyr Val Ala  
260 265 270

Asp Val Tyr Thr Asp Leu Thr Pro Leu Ser Lys Phe Pro Ser Pro Glu  
275 280 285

Tyr Glu Thr Phe Ala Glu Tyr Tyr Lys Thr Lys Tyr Asn Leu Asp Leu  
290 295 300

Thr Asn Leu Asn Gln Pro Leu Leu Asp Val Asp His Thr Ser Ser Arg  
305 310 315 320

## 664674description (1)Sequence Listing

Leu Asn Leu Leu Thr Pro Arg His Leu Asn Gln Lys Gly Lys Ala Leu  
 325 330 335

Pro Leu Ser Ser Ala Glu Lys Arg Lys Ala Lys Trp Glu Ser Leu Gln  
 340 345 350

Asn Lys Gln Ile Leu Val Pro Glu Leu Cys Ala Ile His Pro Ile Pro  
 355 360 365

Ala Ser Leu Trp Arg Lys Ala Val Cys Leu Pro Ser Ile Leu Tyr Arg  
 370 375 380

Leu His Cys Leu Leu Thr Ala Glu Glu Leu Arg Ala Gln Thr Ala Ser  
 385 390 395 400

Asp Ala Gly Val Gly Val Arg Ser Leu Pro Ala Asp Phe Arg Tyr Pro  
 405 410 415

Asn Leu Asp Phe Gly Trp Lys Lys Ser Ile Asp Ser Lys Ser Phe Ile  
 420 425 430

Ser Ile Ser Asn Ser Ser Ser Ala Glu Asn Asp Asn Tyr Cys Lys His  
 435 440 445

Ser Thr Ile Val Pro Glu Asn Ala Ala His Gln Gly Ala Asn Arg Thr  
 450 455 460

Ser Ser Leu Glu Asn His Asp Gln Met Ser Val Asn Cys Arg Thr Leu  
 465 470 475 480

Leu Ser Glu Ser Pro Gly Lys Leu His Val Glu Val Ser Ala Asp Leu  
 485 490 495

Thr Ala Ile Asn Gly Leu Ser Tyr Asn Gln Asn Leu Ala Asn Gly Ser  
 500 505 510

Tyr Asp Leu Ala Asn Arg Asp Phe Cys Gln Gly Asn Gln Leu Asn Tyr  
 515 520 525

Tyr Lys Gln Glu Ile Pro Val Gln Pro Thr Thr Ser Tyr Ser Ile Gln  
 530 535 540

664674description (1)Sequence Listing

Asn Leu Tyr Ser Tyr Glu Asn Gln Pro Gln Pro Ser Asp Glu Cys Thr  
545 550 555 560

Leu Leu Ser Asn Lys Tyr Leu Asp Gly Asn Ala Asn Lys Ser Thr Ser  
565 570 575

Asp Gly Ser Pro Val Met Ala Val Met Pro Gly Thr Thr Asp Thr Ile  
580 585 590

Gln Val Leu Lys Gly Arg Met Asp Ser Glu Gln Ser Pro Ser Ile Gly  
595 600 605

Tyr Ser Ser Arg Thr Leu Gly Pro Asn Pro Gly Leu Ile Leu Gln Ala  
610 615 620

Leu Thr Leu Ser Asn Ala Ser Asp Gly Phe Asn Leu Glu Arg Leu Glu  
625 630 635 640

Met Leu Gly Asp Ser Phe Leu Lys His Ala Ile Thr Thr Tyr Leu Phe  
645 650 655

Cys Thr Tyr Pro Asp Ala His Glu Gly Arg Leu Ser Tyr Met Arg Ser  
660 665 670

Lys Lys Val Ser Asn Cys Asn Leu Tyr Arg Leu Gly Lys Lys Lys Gly  
675 680 685

Leu Pro Ser Arg Met Val Val Ser Ile Phe Asp Pro Pro Val Asn Trp  
690 695 700

Leu Pro Pro Gly Tyr Val Val Asn Gln Asp Lys Ser Asn Thr Asp Lys  
705 710 715 720

Trp Glu Lys Asp Glu Met Thr Lys Asp Cys Met Leu Ala Asn Gly Lys  
725 730 735

Leu Asp Glu Asp Tyr Glu Glu Glu Asp Glu Glu Glu Glu Ser Leu Met  
740 745 750

Trp Arg Ala Pro Lys Glu Glu Ala Asp Tyr Glu Asp Asp Phe Leu Glu  
755 760 765

## 664674description (1)Sequence Listing

Tyr Asp Gln Glu His Ile Arg Phe Ile Asp Asn Met Leu Met Gly Ser  
 770 775 780

Gly Ala Phe Val Lys Lys Ile Ser Leu Ser Pro Phe Ser Thr Thr Asp  
 785 790 795 800

Ser Ala Tyr Glu Trp Lys Met Pro Lys Lys Ser Ser Leu Gly Ser Met  
 805 810 815

Pro Phe Ser Ser Asp Phe Glu Asp Phe Asp Tyr Ser Ser Trp Asp Ala  
 820 825 830

Met Cys Tyr Leu Asp Pro Ser Lys Ala Val Glu Glu Asp Asp Phe Val  
 835 840 845

Val Gly Phe Trp Asn Pro Ser Glu Glu Asn Cys Gly Val Asp Thr Gly  
 850 855 860

Lys Gln Ser Ile Ser Tyr Asp Leu His Thr Glu Gln Cys Ile Ala Asp  
 865 870 875 880

Lys Ser Ile Ala Asp Cys Val Glu Ala Leu Leu Gly Cys Tyr Leu Thr  
 885 890 895

Ser Cys Gly Glu Arg Ala Ala Gln Leu Phe Leu Cys Ser Leu Gly Leu  
 900 905 910

Lys Val Leu Pro Val Ile Lys Arg Thr Asp Arg Glu Lys Ala Leu Cys  
 915 920 925

Pro Thr Arg Glu Asn Phe Asn Ser Gln Gln Lys Asn Leu Ser Val Ser  
 930 935 940

Cys Ala Ala Ala Ser Val Ala Ser Ser Arg Ser Ser Val Leu Lys Asp  
 945 950 955 960

Ser Glu Tyr Gly Cys Leu Lys Ile Pro Pro Arg Cys Met Phe Asp His  
 965 970 975

Pro Asp Ala Asp Lys Thr Leu Asn His Leu Ile Ser Gly Phe Glu Asn  
 980 985 990



664674description (1)Sequence Listing

Phe Glu Lys Lys Ile Asn Tyr Arg Phe Lys Asn Lys Ala Tyr Leu Leu  
 995 1000 1005

Gln Ala Phe Thr His Ala Ser Tyr His Tyr Asn Thr Ile Thr Asp  
 1010 1015 1020

Cys Tyr Gln Arg Leu Glu Phe Leu Gly Asp Ala Ile Leu Asp Tyr  
 1025 1030 1035

Leu Ile Thr Lys His Leu Tyr Glu Asp Pro Arg Gln His Ser Pro  
 1040 1045 1050

Gly Val Leu Thr Asp Leu Arg Ser Ala Leu Val Asn Asn Thr Ile  
 1055 1060 1065

Phe Ala Ser Leu Ala Val Lys Tyr Asp Tyr His Lys Tyr Phe Lys  
 1070 1075 1080

Ala Val Ser Pro Glu Leu Phe His Val Ile Asp Asp Phe Val Gln  
 1085 1090 1095

Phe Gln Leu Glu Lys Asn Glu Met Gln Gly Met Asp Ser Glu Leu  
 1100 1105 1110

Arg Arg Ser Glu Glu Asp Glu Glu Lys Glu Glu Asp Ile Glu Val  
 1115 1120 1125

Pro Lys Ala Met Gly Asp Ile Phe Glu Ser Leu Ala Gly Ala Ile  
 1130 1135 1140

Tyr Met Asp Ser Gly Met Ser Leu Glu Thr Val Trp Gln Val Tyr  
 1145 1150 1155

Tyr Pro Met Met Arg Pro Leu Ile Glu Lys Phe Ser Ala Asn Val  
 1160 1165 1170

Pro Arg Ser Pro Val Arg Glu Leu Leu Glu Met Glu Pro Glu Thr  
 1175 1180 1185

Ala Lys Phe Ser Pro Ala Glu Arg Thr Tyr Asp Gly Lys Val Arg  
 1190 1195 1200

664674description (1)Sequence Listing

Val Thr Val Glu Val Val Gly Lys Gly Lys Phe Lys Gly Val Gly  
1205 1210 1215

Arg Ser Tyr Arg Ile Ala Lys Ser Ala Ala Ala Arg Arg Ala Leu  
1220 1225 1230

Arg Ser Leu Lys Ala Asn Gln Pro Gln Val Pro Asn Ser  
1235 1240 1245

<210> 18  
<211> 1267  
<212> PRT  
<213> Artificial

<220>  
<223> An amino acid sequence of human dicer mutant

<400> 18

Met Asn His Lys Val His His His His His His Ile Glu Gly Arg Asn  
1 5 10 15

Ser Ser Ser Val Pro Ala Ser Ile Val Gly Pro Pro Met Ser Cys Val  
20 25 30

Arg Leu Ala Glu Arg Val Val Ala Leu Ile Cys Cys Glu Lys Leu His  
35 40 45

Lys Ile Gly Glu Leu Asp Asp His Leu Met Pro Val Gly Lys Glu Thr  
50 55 60

Val Lys Tyr Glu Glu Glu Leu Asp Leu His Asp Glu Glu Glu Thr Ser  
65 70 75 80

Val Pro Gly Arg Pro Gly Ser Thr Lys Arg Arg Gln Cys Tyr Pro Lys  
85 90 95

Ala Ile Pro Glu Cys Leu Arg Asp Ser Tyr Pro Arg Pro Asp Gln Pro  
100 105 110

Cys Tyr Leu Tyr Val Ile Gly Met Val Leu Thr Thr Pro Leu Pro Asp  
115 120 125

Glu Leu Asn Phe Arg Arg Arg Lys Leu Tyr Pro Pro Glu Asp Thr Thr  
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## 664674description (1)Sequence Listing

130

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140

Arg Cys Phe Gly Ile Leu Thr Ala Lys Pro Ile Pro Gln Ile Pro His  
 145 150 155 160

Phe Pro Val Tyr Thr Arg Ser Gly Glu Val Thr Ile Ser Ile Glu Leu  
 165 170 175

Lys Lys Ser Gly Phe Met Leu Ser Leu Gln Met Leu Glu Leu Ile Thr  
 180 185 190

Arg Leu His Gln Tyr Ile Phe Ser His Ile Leu Arg Leu Glu Lys Pro  
 195 200 205

Ala Leu Glu Phe Lys Pro Thr Asp Ala Asp Ser Ala Tyr Cys Val Leu  
 210 215 220

Pro Leu Asn Val Val Asn Asp Ser Ser Thr Leu Asp Ile Asp Phe Lys  
 225 230 235 240

Phe Met Glu Asp Ile Glu Lys Ser Glu Ala Arg Ile Gly Ile Pro Ser  
 245 250 255

Thr Lys Tyr Thr Lys Glu Thr Pro Phe Val Phe Lys Leu Glu Asp Tyr  
 260 265 270

Gln Asp Ala Val Ile Ile Pro Arg Tyr Arg Asn Phe Asp Gln Pro His  
 275 280 285

Arg Phe Tyr Val Ala Asp Val Tyr Thr Asp Leu Thr Pro Leu Ser Lys  
 290 295 300

Phe Pro Ser Pro Glu Tyr Glu Thr Phe Ala Glu Tyr Tyr Lys Thr Lys  
 305 310 315 320

Tyr Asn Leu Asp Leu Thr Asn Leu Asn Gln Pro Leu Leu Asp Val Asp  
 325 330 335

His Thr Ser Ser Arg Leu Asn Leu Leu Thr Pro Arg His Leu Asn Gln  
 340 345 350

Lys Gly Lys Ala Leu Pro Leu Ser Ser Ala Glu Lys Arg Lys Ala Lys

664674description (1)Sequence Listing

355  
 Trp Glu Ser Leu Gln Asn Lys Gln Ile Leu Val Pro Glu Leu Cys Ala  
 370 375 380

Ile His Pro Ile Pro Ala Ser Leu Trp Arg Lys Ala Val Cys Leu Pro  
 385 390 395 400

Ser Ile Leu Tyr Arg Leu His Cys Leu Leu Thr Ala Glu Glu Leu Arg  
 405 410 415

Ala Gln Thr Ala Ser Asp Ala Gly Val Gly Val Arg Ser Leu Pro Ala  
 420 425 430

Asp Phe Arg Tyr Pro Asn Leu Asp Phe Gly Trp Lys Lys Ser Ile Asp  
 435 440 445

Ser Lys Ser Phe Ile Ser Ile Ser Asn Ser Ser Ser Ala Glu Asn Asp  
 450 455 460

Asn Tyr Cys Lys His Ser Thr Ile Val Pro Glu Asn Ala Ala His Gln  
 465 470 475 480

Gly Ala Asn Arg Thr Ser Ser Leu Glu Asn His Asp Gln Met Ser Val  
 485 490 495

Asn Cys Arg Thr Leu Leu Ser Glu Ser Pro Gly Lys Leu His Val Glu  
 500 505 510

Val Ser Ala Asp Leu Thr Ala Ile Asn Gly Leu Ser Tyr Asn Gln Asn  
 515 520 525

Leu Ala Asn Gly Ser Tyr Asp Leu Ala Asn Arg Asp Phe Cys Gln Gly  
 530 535 540

Asn Gln Leu Asn Tyr Tyr Lys Gln Glu Ile Pro Val Gln Pro Thr Thr  
 545 550 555 560

Ser Tyr Ser Ile Gln Asn Leu Tyr Ser Tyr Glu Asn Gln Pro Gln Pro  
 565 570 575

Ser Asp Glu Cys Thr Leu Leu Ser Asn Lys Tyr Leu Asp Gly Asn Ala

## 664674description (1)Sequence Listing

580

585

590

Asn Lys Ser Thr Ser Asp Gly Ser Pro Val Met Ala Val Met Pro Gly  
595 600 605

Thr Thr Asp Thr Ile Gln Val Leu Lys Gly Arg Met Asp Ser Glu Gln  
610 615 620

Ser Pro Ser Ile Gly Tyr Ser Ser Arg Thr Leu Gly Pro Asn Pro Gly  
625 630 635 640

Leu Ile Leu Gln Ala Leu Thr Leu Ser Asn Ala Ser Asp Gly Phe Asn  
645 650 655

Leu Glu Arg Leu Glu Met Leu Gly Asp Ser Phe Leu Lys His Ala Ile  
660 665 670

Thr Thr Tyr Leu Phe Cys Thr Tyr Pro Asp Ala His Glu Gly Arg Leu  
675 680 685

Ser Tyr Met Arg Ser Lys Lys Val Ser Asn Cys Asn Leu Tyr Arg Leu  
690 695 700

Gly Lys Lys Lys Gly Leu Pro Ser Arg Met Val Val Ser Ile Phe Asp  
705 710 715 720

Pro Pro Val Asn Trp Leu Pro Pro Gly Tyr Val Val Asn Gln Asp Lys  
725 730 735

Ser Asn Thr Asp Lys Trp Glu Lys Asp Glu Met Thr Lys Asp Cys Met  
740 745 750

Leu Ala Asn Gly Lys Leu Asp Glu Asp Tyr Glu Glu Glu Asp Glu Glu  
755 760 765

Glu Glu Ser Leu Met Trp Arg Ala Pro Lys Glu Glu Ala Asp Tyr Glu  
770 775 780

Asp Asp Phe Leu Glu Tyr Asp Gln Glu His Ile Arg Phe Ile Asp Asn  
785 790 795 800

Met Leu Met Gly Ser Gly Ala Phe Val Lys Lys Ile Ser Leu Ser Pro  
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664674description (1)Sequence Listing

805 Phe Ser Thr Thr Asp Ser Ala Tyr Glu Trp Lys Met Pro Lys Lys Ser  
 820 825 830  
 Ser Leu Gly Ser Met Pro Phe Ser Ser Asp Phe Glu Asp Phe Asp Tyr  
 835 840 845  
 Ser Ser Trp Asp Ala Met Cys Tyr Leu Asp Pro Ser Lys Ala Val Glu  
 850 855 860  
 Glu Asp Asp Phe Val Val Gly Phe Trp Asn Pro Ser Glu Glu Asn Cys  
 865 870 875 880  
 Gly Val Asp Thr Gly Lys Gln Ser Ile Ser Tyr Asp Leu His Thr Glu  
 885 890 895  
 Gln Cys Ile Ala Asp Lys Ser Ile Ala Asp Cys Val Glu Ala Leu Leu  
 900 905 910  
 Gly Cys Tyr Leu Thr Ser Cys Gly Glu Arg Ala Ala Gln Leu Phe Leu  
 915 920 925  
 Cys Ser Leu Gly Leu Lys Val Leu Pro Val Ile Lys Arg Thr Asp Arg  
 930 935 940  
 Glu Lys Ala Leu Cys Pro Thr Arg Glu Asn Phe Asn Ser Gln Gln Lys  
 945 950 955 960  
 Asn Leu Ser Val Ser Cys Ala Ala Ala Ser Val Ala Ser Ser Arg Ser  
 965 970 975  
 Ser Val Leu Lys Asp Ser Glu Tyr Gly Cys Leu Lys Ile Pro Pro Arg  
 980 985 990  
 Cys Met Phe Asp His Pro Asp Ala Asp Lys Thr Leu Asn His Leu Ile  
 995 1000 1005  
 Ser Gly Phe Glu Asn Phe Glu Lys Lys Ile Asn Tyr Arg Phe Lys  
 1010 1015 1020  
 Asn Lys Ala Tyr Leu Leu Gln Ala Phe Thr His Ala Ser Tyr His

## 1025

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1200

1205

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121

1220

1225

123

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## 664674description (1)Sequence Listing

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1245

Ala Ala Arg Arg Ala Leu Arg Ser Leu Lys Ala Asn Gln Pro Gln  
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Val Pro Asn Ser  
 1265

<210> 19  
 <211> 3804  
 <212> DNA  
 <213> Artificial

<220>  
 <223> A gene encoding human dicer mutant

<400> 19  
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 ctcatattgct gtgagaaact gcacaaaatt ggcgaaactgg atgaccattt gatgccagtt 180  
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 tgtttgaggg atagttatcc cagacctgat cagccctgtt acctgtatgt gataggaatg 360  
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 gaagatacca caagatgctt tggaatactg acggccaaac ccataacctca gattccacac 480  
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 agacttaatc ttttgacacc togacatttg aatcagaagg ggaaagcgct tcctttaago 1080



## 664674description (1)Sequence Listing

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gaactctgtg ctatacatcc aattccagca tcaactgtga gaaaagctgt ttgtctcccc	1200
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cctgtgatgg ccgtaatgcc tggtagaca gacactattc aagtgtcaa gggcaggatg	1860
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gaaatgcttg gcgactcctt tttaaagcat gccatcacca catatctatt ttgcacttac	2040
cctgatgcgc atgagggccg cctttcatat atgagaagca aaaaggctcag caactgtaat	2100
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gattctgcat atgaatggaa aatgccc aaaatcctct taggtagtat gccattttca	2520
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gacaaaagca tagcggactg tgtggaagcc ctgctgggct gctatttaac cagctgtggg	2760

## 664674description (1)Sequence Listing

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cagcttgaga agaatgaaat gcaaggaatg gattctgagc ttaggagatc tgaggaggat 3420
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664674description (1)Sequence Listing

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<223> Synthetic primer F to amplify a gene encoding CspB

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37